

SEQUENCE LISTING

<110> Alitalo, Kari
Joukov, Vladimir

<120> VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN
AND GENE, MUTANTS THEREOF, AND USES THEREOF

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<151> 1999-11-05

<150> PCT/US98/01973

<151> 1998-02-02

<150> 08/795,430

<151> 1997-02-05

<150> PCT/FI96/00427

<151> 1996-08-01

<150> 08/671,573

<151> 1996-06-28

<150> 08/601,132

<151> 1996-02-14

<150> 08/585,895

<151> 1996-01-12

<150> 08/510,133

<151> 1995-08-01

<150> 08/340,011

<151> 1994-11-14

<160> 59

<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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<223> Human Flt4 cDNA (short form)

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<213> Homo sapiens

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<223> Human Flt4 cDNA (3' end-long form)

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<212> DNA

<213> Artificial Sequence

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4273

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<212> PRT

<213> Homo sapiens

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<223> Flt4 c-terminal peptide

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<213> Artificial Sequence

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Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
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Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
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Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
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tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac 645
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
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agc taagattgta ctgttttcca gttcatcgat tttctattat ggaaaactgt 1658
Ser

gttgccacag tagaactgtc tgtgaacaga gagacccttg tgggtccatg ctaacaaaga 1718
caaaagtctg tctttcctga accatgtgga taactttaca gaaatggact ggagctcatc 1778
tgcaaaaggc ctcttgtaaa gactgggtttt ctgccaatga ccaaacagcc aagattttcc 1838
tcttgtgatt tctttaaaag aatgactata taatttattt ccactaaaaa tattgtttct 1898
gcattcattt ttatagcaac aacaattggt aaaactcact gtgatcaata tttttatatt 1958
atgcaaaaata tgtttaaaat aaaatgaaaa ttgtattat 1997

<210> 8
<211> 419
<212> PRT
<213> Homo sapiens

<400> 8
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
1 5 10 15
Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe
20 25 30
Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
35 40 45
Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60
Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95
Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110
His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
405 410 415

Gln Met Ser

<210> 9
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<223> VEGF-C peptide "PAM126"

<400> 9
Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu
1 5 10 15

Lys

<210> 10
<211> 1836
<212> DNA
<213> Murine

<220>
<221> CDS
<222> (168) .. (1412)

<220>
<223> cDNA encoding murine VEGF-C precursor

<400> 10
gcggccgcgt cgacgcaaaa gttgcgagcc gccgagtcgc gggagacgct cgcccagggg 60
ggccccggg aggaaccac gggacagga ccaggagagg acctcagcct cagccccag 120
cctgcgccag ccaacggacc ggctccctg ctcccggtcc atccacc atg cac ttg 176
Met His Leu
1
ctg tgc ttc ttg tct ctg gcg tgt tcc ctg ctc gcc gct gcg ctg atc 224
Leu Cys Phe Leu Ser Leu Ala Cys Ser Leu Leu Ala Ala Ala Leu Ile
5 10 15
ccc agt ccg cgc gag gcg ccc gcc acc gtc gcc gcc ttc gag tcg gga 272
Pro Ser Pro Arg Glu Ala Pro Ala Thr Val Ala Ala Phe Glu Ser Gly
20 25 30 35
ctg ggc ttc tcg gaa gcg gag ccc gac ggg ggc gag gtc aag gct ttt 320
Leu Gly Phe Ser Glu Ala Glu Pro Asp Gly Gly Glu Val Lys Ala Phe
40 45 50

gaa ggc aaa gac ctg gag gag cag ttg cgg tct gtg tcc agc gta gat	368
Glu Gly Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val Asp	
55 60 65	
gag ctg atg tct gtc ctg tac cca gac tac tgg aaa atg tac aag tgc	416
Glu Leu Met Ser Val Leu Tyr Pro Asp Tyr Trp Lys Met Tyr Lys Cys	
70 75 80	
cag ctg cgg aaa ggc ggc tgg cag cag ccc acc ctc aat acc agg aca	464
Gln Leu Arg Lys Gly Gly Trp Gln Gln Pro Thr Leu Asn Thr Arg Thr	
85 90 95	
ggg gac agt gta aaa ttt gct gct gca cat tat aac aca gag atc ctg	512
Gly Asp Ser Val Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu	
100 105 110 115	
aaa agt att gat aat gag tgg aga aag act caa tgc atg cca cgt gag	560
Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu	
120 125 130	
gtg tgt ata gat gtg ggg aag gag ttt gga gca gcc aca aac acc ttc	608
Val Cys Ile Asp Val Gly Lys Glu Phe Gly Ala Ala Thr Asn Thr Phe	
135 140 145	
ttt aaa cct cca tgt gtg tcc gtc tac aga tgt ggg ggt tgc tgc aac	656
Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn	
150 155 160	
agc gag ggg ctg cag tgc atg aac acc agc aca ggt tac ctc agc aag	704
Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Gly Tyr Leu Ser Lys	
165 170 175	
acg ttg ttt gaa att aca gtg cct ctc tca caa ggc ccc aaa cca gtc	752
Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys Pro Val	
180 185 190 195	
aca atc agt ttt gcc aat cac act tcc tgc cgg tgc atg tct aaa ctg	800
Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu	
200 205 210	
gat gtt tac aga caa gtt cat tca att att aga cgt tct ctg cca gca	848
Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu Pro Ala	
215 220 225	
aca tta cca cag tgt cag gca gct aac aag aca tgt cca aca aac tat	896
Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr	
230 235 240	
gtg tgg aat aac tac atg tgc cga tgc ctg gct cag cag gat ttt atc	944
Val Trp Asn Asn Tyr Met Cys Arg Cys Leu Ala Gln Gln Asp Phe Ile	
245 250 255	
ttt tat tca aat gtt gaa gat gac tca acc aat gga ttc cat gat gtc	992
Phe Tyr Ser Asn Val Glu Asp Asp Ser Thr Asn Gly Phe His Asp Val	
260 265 270 275	

tgt gga ccc aac aag gag ctg gat gaa gac acc tgt cag tgt gtc tgc 1040
 Cys Gly Pro Asn Lys Glu Leu Asp Glu Asp Thr Cys Gln Cys Val Cys
 280 285 290

aag ggg ggg ctt cgg cca tct agt tgt gga ccc cac aaa gaa cta gat 1088
 Lys Gly Gly Leu Arg Pro Ser Ser Cys Gly Pro His Lys Glu Leu Asp
 295 300 305

aga gac tca tgt cag tgt gtc tgt aaa aac aaa ctt ttc cct aat tca 1136
 Arg Asp Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe Pro Asn Ser
 310 315 320

tgt gga gcc aac agg gaa ttt gat gag aat aca tgt cag tgt gta tgt 1184
 Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln Cys Val Cys
 325 330 335

aaa aga acg tgt cca aga aat cag ccc ctg aat cct ggg aaa tgt gcc 1232
 Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala
 340 345 350 355

tgt gaa tgt aca gaa aac aca cag aag tgc ttc ctt aaa ggg aag aag 1280
 Cys Glu Cys Thr Glu Asn Thr Gln Lys Cys Phe Leu Lys Gly Lys Lys
 360 365 370

ttc cac cat caa aca tgc agt tgt tac aga aga ccg tgt gcg aat cga 1328
 Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys Ala Asn Arg
 375 380 385

ctg aag cat tgt gat cca gga ctg tcc ttt agt gaa gaa gta tgc cgc 1376
 Leu Lys His Cys Asp Pro Gly Leu Ser Phe Ser Glu Glu Val Cys Arg
 390 395 400

tgt gtc cca tcg tat tgg aaa agg cca cat ctg aac taagatcata 1422
 Cys Val Pro Ser Tyr Trp Lys Arg Pro His Leu Asn
 405 410 415

ccagttttca gtcagtcaca gtcatttact ctcttgaaga ctgttggaac agcacttagc 1482

actgtctatg cacagaaaga ctctgtggga ccacatggta acagaggccc aagtctgtgt 1542

ttattgaacc atgtggatta ctgcgggaga ggactggcac tcatgtgcaa aaaaaacctc 1602

ttcaaagact ggttttctgc cagggaccag acagctgagg tttttctctt gtgatttata 1662

aaaagaatga ctatataatt tatttccact aaaaatattg ttctgcatt catttttata 1722

gcaataacaa ttggtaaagc tcaactgtgat cagtattttt ataacatgca aaactatggt 1782

taaaataaaa tgaaaattgt attataaaaa aaaaaaaaaa aaaaaaaaaa gctt 1836

<210> 11
 <211> 415
 <212> PRT
 <213> Murine

<400> 11
Met His Leu Leu Cys Phe Leu Ser Leu Ala Cys Ser Leu Leu Ala Ala
1 5 10 15
Ala Leu Ile Pro Ser Pro Arg Glu Ala Pro Ala Thr Val Ala Ala Phe
20 25 30
Glu Ser Gly Leu Gly Phe Ser Glu Ala Glu Pro Asp Gly Gly Glu Val
35 40 45
Lys Ala Phe Glu Gly Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60
Ser Val Asp Glu Leu Met Ser Val Leu Tyr Pro Asp Tyr Trp Lys Met
65 70 75 80
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln Gln Pro Thr Leu Asn
85 90 95
Thr Arg Thr Gly Asp Ser Val Lys Phe Ala Ala Ala His Tyr Asn Thr
100 105 110
Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met
115 120 125
Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Ala Ala Thr
130 135 140
Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly
145 150 155 160
Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Gly Tyr
165 170 175
Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro
180 185 190
Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met
195 200 205
Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser
210 215 220
Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr Cys Pro
225 230 235 240
Thr Asn Tyr Val Trp Asn Asn Tyr Met Cys Arg Cys Leu Ala Gln Gln
245 250 255
Asp Phe Ile Phe Tyr Ser Asn Val Glu Asp Asp Ser Thr Asn Gly Phe
260 265 270
His Asp Val Cys Gly Pro Asn Lys Glu Leu Asp Glu Asp Thr Cys Gln
275 280 285

Cys Val Cys Lys Gly Gly Leu Arg Pro Ser Ser Cys Gly Pro His Lys
290 295 300

Glu Leu Asp Arg Asp Ser Cys Gln Cys Val Cys Lys Asn Lys Leu Phe
305 310 315 320

Pro Asn Ser Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr Cys Gln
325 330 335

Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn Pro Gly
340 345 350

Lys Cys Ala Cys Glu Cys Thr Glu Asn Thr Gln Lys Cys Phe Leu Lys
355 360 365

Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg Pro Cys
370 375 380

Ala Asn Arg Leu Lys His Cys Asp Pro Gly Leu Ser Phe Ser Glu Glu
385 390 395 400

Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro His Leu Asn
405 410 415

<210> 12
<211> 1741
<212> DNA
<213> Quail

<220>
<221> CDS
<222> (453) .. (1706)

<220>
<223> Quail VEGF-C cDNA

<400> 12
gccccgcgcg agcgctccgc gcgcagccgc cgggcccgggc cggcccgcgcg agggcgcgct 60
gcgagcggcc actgggtcct gcttccctcc ttcctctccc tctctctcct cctccttctc 120
tctgcgcttt ccaccgctcc cgagcgagcg cacgctcgga tgtccgggtt cctgggtgggt 180
tttttacctg gcaaagtccg gataacttcg gtgagaattt gcaaagaggc tgggagctcc 240
cctgcaggcg tctgggagct gctgccgcgc tgcctcttc tccatcccgc ggattttact 300
gccttgata ttgcgagggg agggaggggg gtgaggacag caaaaagaaa ggggtggggg 360
gggggagaga aaaggaaaag aaggagcctc ggaattgtgc ccgcattcct gcgctgcccc 420
ggggccccc tccgctctgc catctccgca ca atg cac ttg ctg gag atg ctc 473
Met His Leu Leu Glu Met Leu

tcc ctg ggc tgc tgc ctc gct gct ggc gcc gtg ctc ctg gga ccc cgg	521
Ser Leu Gly Cys Cys Leu Ala Ala Gly Ala Val Leu Leu Gly Pro Arg	
10 15 20	
cag ccg ccc gtc gcc gcc gcc tac gag tcc ggg cac ggc tac tac gag	569
Gln Pro Pro Val Ala Ala Ala Tyr Glu Ser Gly His Gly Tyr Tyr Glu	
25 30 35	
gag gag ccc ggt gcc ggg gaa ccc aag gct cat gca agc aaa gac ctg	617
Glu Glu Pro Gly Ala Gly Glu Pro Lys Ala His Ala Ser Lys Asp Leu	
40 45 50 55	
gaa gag cag ttg cga tct gtg tcc agt gtg gat gaa ctc atg aca gta	665
Glu Glu Gln Leu Arg Ser Val Ser Ser Val Asp Glu Leu Met Thr Val	
60 65 70	
ctt tac cca gaa tac tgg aaa atg ttc aaa tgt cag ttg agg aaa gga	713
Leu Tyr Pro Glu Tyr Trp Lys Met Phe Lys Cys Gln Leu Arg Lys Gly	
75 80 85	
ggg tgg caa cac aac agg gaa cac tcc agc tct gat aca aga tca gat	761
Gly Trp Gln His Asn Arg Glu His Ser Ser Ser Asp Thr Arg Ser Asp	
90 95 100	
gat tca ttg aaa ttt gcc gca gca cat tat aat gca gag atc ctg aaa	809
Asp Ser Leu Lys Phe Ala Ala Ala His Tyr Asn Ala Glu Ile Leu Lys	
105 110 115	
agt att gat act gaa tgg aga aaa acc cag ggc atg cca cgt gaa gtg	857
Ser Ile Asp Thr Glu Trp Arg Lys Thr Gln Gly Met Pro Arg Glu Val	
120 125 130 135	
tgt gtg gat ttg ggg aaa gag ttt gga gca act aca aac acc ttc ttt	905
Cys Val Asp Leu Gly Lys Glu Phe Gly Ala Thr Thr Asn Thr Phe Phe	
140 145 150	
aaa ccc ccg tgt gta tcc atc tac aga tgt gga ggt tgc tgc aat agt	953
Lys Pro Pro Cys Val Ser Ile Tyr Arg Cys Gly Gly Cys Cys Asn Ser	
155 160 165	
gaa gga ctc cag tgt atg aat atc agc aca aat tac atc agc aag aca	1001
Glu Gly Leu Gln Cys Met Asn Ile Ser Thr Asn Tyr Ile Ser Lys Thr	
170 175 180	
ttg ttt gag att aca gtg cct ctc tct cat ggc ccc aaa cct gta aca	1049
Leu Phe Glu Ile Thr Val Pro Leu Ser His Gly Pro Lys Pro Val Thr	
185 190 195	
gtc agt ttt gcc aat cac acg tcc tgc cga tgc atg tct aag ttg gat	1097
Val Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp	
200 205 210 215	
gtt tac aga caa gtt cat tct atc ata aga cgt tcc ttg cca gca aca	1145
Val Tyr Arg Gln Val His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr	
220 225 230	

caa act cag tgt cat gtg gca aac aag acc tgt cca aaa aat cat gtc 1193
 Gln Thr Gln Cys His Val Ala Asn Lys Thr Cys Pro Lys Asn His Val
 235 240 245

tgg aat aat cag att tgc aga tgc tta gca cag cac gat ttt ggt ttc 1241
 Trp Asn Asn Gln Ile Cys Arg Cys Leu Ala Gln His Asp Phe Gly Phe
 250 255 260

tct tct cac ctt gga gat tct gac aca tct gaa gga ttc cat att tgt 1289
 Ser Ser His Leu Gly Asp Ser Asp Thr Ser Glu Gly Phe His Ile Cys
 265 270 275

ggg ccc aac aaa gag ctg gat gaa gaa acc tgt caa tgc gtc tgc aaa 1337
 Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Lys
 280 285 290 295

gga ggt gtg cgg ccc ata agc tgt ggc cct cac aaa gaa cta gac agg 1385
 Gly Gly Val Arg Pro Ile Ser Cys Gly Pro His Lys Glu Leu Asp Arg
 300 305 310

gca tca tgt cag tgc atg tgc aaa aac aaa ctg ctc ccc agt tcc tgt 1433
 Ala Ser Cys Gln Cys Met Cys Lys Asn Lys Leu Leu Pro Ser Ser Cys
 315 320 325

ggg cct aac aaa gaa ttt gat gaa gaa aag tgc cag tgt gta tgt aaa 1481
 Gly Pro Asn Lys Glu Phe Asp Glu Glu Lys Cys Gln Cys Val Cys Lys
 330 335 340

aag acc tgt ccc aaa cat cat cca cta aat cct gca aaa tgc atc tgc 1529
 Lys Thr Cys Pro Lys His His Pro Leu Asn Pro Ala Lys Cys Ile Cys
 345 350 355

gaa tgt aca gaa tct ccc aat aaa tgt ttc tta aaa gga aaa aga ttt 1577
 Glu Cys Thr Glu Ser Pro Asn Lys Cys Phe Leu Lys Gly Lys Arg Phe
 360 365 370 375

cat cac cag aca tgc agt tgt tac aga cca cca tgt aca gtc cga acg 1625
 His His Gln Thr Cys Ser Cys Tyr Arg Pro Pro Cys Thr Val Arg Thr
 380 385 390

aaa cgc tgt gat gct gga ttt ctg tta gct gaa gaa gtg tgc cgc tgt 1673
 Lys Arg Cys Asp Ala Gly Phe Leu Leu Ala Glu Glu Val Cys Arg Cys
 395 400 405

gta cgc aca tct tgg aaa aga cca ctt atg aat taagcgaaga aagcactact 1726
 Val Arg Thr Ser Trp Lys Arg Pro Leu Met Asn
 410 415

cgctatatag tgtcg 1741

<210> 13
 <211> 418
 <212> PRT
 <213> Quail

<400> 13

Met His Leu Leu Glu Met Leu Ser Leu Gly Cys Cys Leu Ala Ala Gly
1 5 10 15

Ala Val Leu Leu Gly Pro Arg Gln Pro Pro Val Ala Ala Ala Tyr Glu
20 25 30

Ser Gly His Gly Tyr Tyr Glu Glu Glu Pro Gly Ala Gly Glu Pro Lys
35 40 45

Ala His Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser
50 55 60

Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Phe
65 70 75 80

Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu His Ser
85 90 95

Ser Ser Asp Thr Arg Ser Asp Asp Ser Leu Lys Phe Ala Ala Ala His
100 105 110

Tyr Asn Ala Glu Ile Leu Lys Ser Ile Asp Thr Glu Trp Arg Lys Thr
115 120 125

Gln Gly Met Pro Arg Glu Val Cys Val Asp Leu Gly Lys Glu Phe Gly
130 135 140

Ala Thr Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Ile Tyr Arg
145 150 155 160

Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Ile Ser
165 170 175

Thr Asn Tyr Ile Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser
180 185 190

His Gly Pro Lys Pro Val Thr Val Ser Phe Ala Asn His Thr Ser Cys
195 200 205

Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile
210 215 220

Arg Arg Ser Leu Pro Ala Thr Gln Thr Gln Cys His Val Ala Asn Lys
225 230 235 240

Thr Cys Pro Lys Asn His Val Trp Asn Asn Gln Ile Cys Arg Cys Leu
245 250 255

Ala Gln His Asp Phe Gly Phe Ser Ser His Leu Gly Asp Ser Asp Thr
260 265 270

Ser Glu Gly Phe His Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu
275 280 285

Thr Cys Gln Cys Val Cys Lys Gly Gly Val Arg Pro Ile Ser Cys Gly
 290 295 300

Pro His Lys Glu Leu Asp Arg Ala Ser Cys Gln Cys Met Cys Lys Asn
 305 310 315 320

Lys Leu Leu Pro Ser Ser Cys Gly Pro Asn Lys Glu Phe Asp Glu Glu
 325 330 335

Lys Cys Gln Cys Val Cys Lys Lys Thr Cys Pro Lys His His Pro Leu
 340 345 350

Asn Pro Ala Lys Cys Ile Cys Glu Cys Thr Glu Ser Pro Asn Lys Cys
 355 360 365

Phe Leu Lys Gly Lys Arg Phe His His Gln Thr Cys Ser Cys Tyr Arg
 370 375 380

Pro Pro Cys Thr Val Arg Thr Lys Arg Cys Asp Ala Gly Phe Leu Leu
 385 390 395 400

Ala Glu Glu Val Cys Arg Cys Val Arg Thr Ser Trp Lys Arg Pro Leu
 405 410 415

Met Asn

<210> 14
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<220>
 <223> IgG-Kappa sequence

<400> 14
 Ala Val Val Met Thr Gln Thr Pro Ala Ser
 1 5 10

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 15
 tctcttctgt gcttgagttg ag

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 16
tctcttctgt ccctgagttg ag

22

<210> 17
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 17
tgtgctgcag caaatTTtat agtctcttct gtggcggcgg cggcggcggg cgcctcgca 60
ggacc 65

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 18
ctggcaggga actgctaata atggaatgaa

30

<210> 19
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 19
gggctccgcg tccgagaggt cgagtccgga ctcgtgatgg tgatggtgat gggcggcggc 60
ggcggcgggc gcctcgcgag gacc 84

<210> 20
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 20
gtattataat gtcctccacc aaattttata g 31

<210> 21
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 21
gttcgctgcc tgacactgtg gtagtggtgc tggcggccgc tagtgatggt gatggtgatg 60
aataatggaa tgaacttgtc tgtaaacatc cag 93

<210> 22
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 22
catgtacgaa ccgccag 17

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 23
aatgaccaga gagaggcgag 20

<210> 24
<211> 24

<212> DNA
<213> Homo sapiens

<400> 24
ggcgaggcca cggtaggtct gcgt

24

<210> 25
<211> 24
<212> DNA
<213> Homo sapiens

<400> 25
tttctttgac aggcttatgc aagc

24

<210> 26
<211> 24
<212> DNA
<213> Homo sapiens

<400> 26
gagatcttga aaagtaagta tggg

24

<210> 27
<211> 23
<212> DNA
<213> Homo sapiens

<400> 27
atgacttgac aggtattgat aat

23

<210> 28
<211> 23
<212> DNA
<213> Homo sapiens

<400> 28
ctcagcaaga cggtgggtat tgt

23

<210> 29
<211> 25
<212> DNA
<213> Homo sapiens

<400> 29
cccttctttg tagttatttg aaatt

25

<210> 30
<211> 27
<212> DNA

<213> Homo sapiens

<400> 30
acactaccac agtgagtatg aattaaa

27

<210> 31
<211> 24
<212> DNA
<213> Homo sapiens

<400> 31
ttcttcctcaaa ggtgtcaggc agcg

24

<210> 32
<211> 21
<212> DNA
<213> Homo sapiens

<400> 32
gctggagatg gtagcagaat g

21

<210> 33
<211> 23
<212> DNA
<213> Homo sapiens

<400> 33
ctatttgtct agactcaaca gat

23

<210> 34
<211> 22
<212> DNA
<213> Homo sapiens

<400> 34
caaacatgca ggtaagagat cc

22

<210> 35
<211> 24
<212> DNA
<213> Homo sapiens

<400> 35
tggttcctta gctgttacag acgg

24

<210> 36
<211> 24
<212> DNA
<213> Murine

<400> 36 ggcgagggtca aggtagggtgc aagg	24
<210> 37 <211> 26 <212> DNA <213> Murine	
<400> 37 attgtctttg acaggctttt tgaagg	26
<210> 38 <211> 21 <212> DNA <213> Murine	
<400> 38 gagatcctga aaagtaagta g	21
<210> 39 <211> 24 <212> DNA <213> Murine	
<400> 39 tgtgactcga caggtattga taat	24
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<400> 40 ctcagcaaga cggtagggtat	20
<210> 41 <211> 25 <212> DNA <213> Murine	
<400> 41 ttgtcccttg tagttgtttg aaatt	25
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<400> 42	

acattaccac agtgagtatg

20

<210> 43
<211> 26
<212> DNA
<213> Murine

<400> 43
gtctcccca aaggtgtcag gcagct

26

<210> 44
<211> 23
<212> DNA
<213> Murine

<400> 44
aatgttgaag atggttaagta aaa

23

<210> 45
<211> 16
<212> DNA
<213> Murine

<400> 45
tctagactca accaat

16

<210> 46
<211> 22
<212> DNA
<213> Murine

<400> 46
caaacatgca ggtaaggagt gt

22

<210> 47
<211> 24
<212> DNA
<213> Murine

<400> 47
ttttccccta gttgttacag aaga

24

<210> 48
<211> 2991
<212> DNA
<213> Homo sapiens

<220>
<223> Genomic DNA - Sequence upstream of VEGF-C coding

sequence

<400> 48

gttttaagta gagacggggt ttcaccaacg gttgaaaata tttatcatgg tctccctaag 60
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ctcccaaagt gctgggatta caggcgtgag ccaccgtgtc cgaccaacct taagacaaac 180
aactactgca tgattgtttt tggagacctt ttttttattc aaataaattt ttgccagcat 240
tttctgactc aaagtatagc agcaggaaga taacactttt gtgagaaaaa agtttgaata 300
cagcttactg ctgtatttaa atgaaacagt agttaatatg atattaatat attttgata 360
tattttgagt ttgttgattt tccagtcttc acccgctgct aggctgtgg gtgttgaaa 420
tgctgtgtt tctcaatttt gtttgctat tagaatctg atgtccaagc ctactccag 480
ttagaccagt taagccagaa aggcagaagg tgtactcaag catctgtttt ttcaaaatct 540
ccttttgtga tgccaagtgc aatcaaagtt tagaatcatt gtaatagcaa atgggtgaat 600
ggaaactcca cttctatctc aaatcctacc ccagtctgcc cttagctgtt ctcttttcac 660
agatctatca atgtctgaag ataactatgg caggctgac aaatatgcat agagcaggaa 720
gacagcaaga gagtataca ctgacatgt tccaaatcac aaaacatctc aacaggctag 780
atcatggacc gagtctgatg ggatggaatt tcataaagat acataaaaaa gcatcttgga 840
tacagtaaac ttaactccac aaatacaggg gaatttagac gtgactaagt agcagtacat 900
atgaaaaatt attgaggaat tttgttgact ttaagggtag tgtgagtcaa cactgtgatt 960
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gcatgctcat tacagcacta agtaccgagc catgttctca accgcatact tcatgaacat 1080
ggaaagctaa cagtatggtt aaggggggaa actggaactg tcatcttggg gaataaaagg 1140
gatatttagc caggagtaaa gttagcttag ggagaccatg ataaatattt tcaaaatatt 1200
tgaaggactc agttgtggaa gtgagattag atttattgtg taaaactcca ggagtcaaaa 1260
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tttgatgttc tgtactgt tgaaccct tagcgtggc ctctgtaacc tgctcaccct 1560

gccccaaagga ggcagctagc caatgccacc agcccaacgg aaaccccagt gcttttccaa 1620
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cacatctctc tttatcacc cttttttcaa gtaaaccaac ttcttgca gaagtgacaat 1740
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ttccaaaggg atcattagca tccatcccaa cagcctgcac tgcactctga gaactgcggg 1860
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ggggccaggc gtgcgggagg gaggacaaga actcgggagt ggccgaggat aaagcggggg 2040
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cacctctaaa gccgggtccc ccaaccgcca gcccgggac tgaacttgcc cctccggccg 2160
cccgtcccc gcaggggaca ggggcgggga gggagagatc cagagggggg ctgggggagg 2220
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gggctctggc gggtttggag gggctgaaca tcgcggggtg ttctggtgtc cccgccccg 2640
cctctccaaa aagctacacc gacgggacc gggcgggcgt cctccctcgc cctcgcttca 2700
cctcggggc tccgaatgcg gggagctcg atgtccggtt tcctgtgagg cttttacctg 2760
acaccgccc ctttccccg gactggctg ggagggcgcc ctgcaaagt gggaacgcgg 2820
agccccggac ccgctccgc cgctccggc tcgcccagg ggggtcgcc ggaggagccc 2880
gggggagagg gaccaggagg ggcccgcg ctcgagggg cgcgcgcgc cccacccctg 2940
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<210> 49

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 49 20
cacggcttat gcaagcaaag

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 50 20
aacacagttt tccataatag

<210> 51
<211> 19
<212> PRT
<213> Homo sapiens

<400> 51
Leu Ser Lys Thr Val Ser Gly Ser Glu Gln Asp Leu Pro His Glu Leu
1 5 10 15

His Val Glu

<210> 52
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 52 25
gacggacaca gatggagggtt taaag

<210> 53
<211> 196
<212> PRT
<213> Homo sapiens

<220>
<223> Human PDGF-A

<400> 53

Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
 1 5 10 15
 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
 20 25 30
 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
 35 40 45
 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
 50 55 60
 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
 65 70 75 80
 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
 85 90 95
 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
 100 105 110
 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
 115 120 125
 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
 130 135 140
 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
 145 150 155 160
 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
 165 170 175
 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
 180 185 190
 Thr Asp Val Arg
 195

<210> 54

<211> 241

<212> PRT

<213> Homo sapiens

<220>

<223> Human PDGF-B

<400> 54

Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg
 1 5 10 15
 Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met
 20 25 30

- 32 -

Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu
35 40 45
His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met
50 55 60
Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg
65 70 75 80
Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu
85 90 95
Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
100 105 110
Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln
115 120 125
Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
130 135 140
Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
145 150 155 160
Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
165 170 175
Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser
180 185 190
Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
195 200 205
Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
210 215 220
Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly
225 230 235 240
Ala

<210> 55
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<223> Human PIGF

<400> 55
Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
5 10 15
1

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Cys Gly Asp
130 135 140

Ala Val Pro Arg Arg
145

<210> 56

<211> 191

<212> PRT

<213> Homo sapiens

<220>

<223> VEGF165 precursor

<400> 56

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
180 185 190

<210> 57

<211> 188

<212> PRT

<213> Homo sapiens

<220>

<223> VEGF-B167

<400> 57

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
130 135 140

Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145 150 155 160

Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
165 170 175

Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
180 185

<210> 58
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: VEGF-C delta Cys156 mutant

<220>
<223> At position 156, "Xaa" can be anything other than cysteine or can be nothing

<400> 58
Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
1 5 10 15
Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
20 25 30
Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
35 40 45
Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60
Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80
Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95
Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110
His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125
Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140
Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Xaa Val Ser Val Tyr
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
405 410 415

Gln Met Ser

<210> 59
<211> 160
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: VEGF-C delta N delta CHis

<400> 59

Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Thr
20 25 30

Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr Asn Thr Glu Ile Leu
35 40 45

Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln Cys Met Pro Arg Glu
50 55 60

Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val Ala Thr Asn Thr Phe
65 70 75 80

Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn
85 90 95

Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys
100 105 110

Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln Gly Pro Lys Pro Val
115 120 125

Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg Cys Met Ser Lys Leu
130 135 140

Asp Val Tyr Arg Gln Val His Ser Ile Ile His His His His His His
145 150 155 160